SEQUENCE LISTING

SEQ. ID. No. 1

3bf4   3000 bp

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SEQ. ID. No. 2

1b11   723 bp

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SEQ. ID. No. 3

cc49   1507 bp

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58

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SEQ. ID. No. 4
cc43   2605 bp

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SEQ. ID. No. 5
41.1   1288 bp

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SEQ. ID. No. 6
GCAP 2820 bp

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SEQ. ID. No. 7

1b4   1205 bp

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SEQ. ID. No. 8

20sa7   456 bp

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SEQ. ID. No. 9

Genomic Sequence Encoding ZABC1

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SEQ. ID. No. 10

ZABC1 Open reading frame

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SEQ. ID. No. 11

ZABC1 Protein

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SEQ. ID. NO. 12

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SEQ. ID. NO. 13
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25

SEQ ID NO 14
gb|M19533|RATCYCA Rat cyclophilin mRNA, complete cds.
      Length = 743

30 Minus Strand HSPs:

Score = 418 (115.5 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 96/112 (85%), Positives = 96/112 (85%), Strand = Minus / Plus
S = rat CYCLOPHILLIN; q= SEQ ID NO 13.
35 Query: 372 TNCAATATCACCGCAGATGGCGAGCCTTTAGGCCATGTCTCCTTCGAGCTATTTGCAGAC 313
               | | | |||||| || |||||||||| || || | |||| |||||||||| |||||||||
Sbjct: 64 TTCGACATCACGGCTGATGGCGAGCCCTTGGGTCGCGTCTGCTTCGAGCTGTTTGCAGAC 123

Query: 312 AAAGTTCCAAAGACATCAGAAAACTTTCATGGTCTGAGCACTGGAGAGAAAG 261
40 |||||||||||||| |||||||||| || |||||||||||| |||||||
Sbjct: 124 AAAGTTCCAAAGACAGCAGAAAACTTTCGTGCTCTGAGCACTGGGGAGAAAG 175

Score = 236 (65.2 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 52/58 (89%), Positives = 52/58 (89%), Strand = Minus / Plus
45
Query: 117 TGCTGGACTCAACACAAATGGTTCCCAGTTTTTCATCTGCACTGCCAAAATCGAGTGG 60
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Sbjct: 348 TGCTGGACCAAACACAAATGGTTCCCAGTTTTTTATCTGCACTGCCAAGACTGAGTGG 405

50 Score = 177 (48.9 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
Identities = 41/48 (85%), Positives = 41/48 (85%), Strand = Minus / Plus

```
Query:    60 GACTGGATGGCAAGCGTGTGATGTTTGGCAAGGTGCAAGAGGGCATGA 13
             | |||||||||||||| |||| | ||||| ||||||| |||| |||||||
Sbjct:   404 GGCTGGATGGCAAGCATGTGGTCTTTGGGAAGGTGAAAGAAGGCATGA 451
```

5
  Score = 154 (42.6 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
  Identities = 34/38 (89%), Positives = 34/38 (89%), Strand = Minus / Plus

```
Query:   153 AGAACTTCGTTCTGAAACATGCAGGTCCTGGCATCTTG 116
             ||||||||| | |||||| ||| ||||||||||||||||
Sbjct:   299 AGAACTTCATCCTGAAGCATACAGGTCCTGGCATCTTG 336
```

10

  Score = 86 (23.8 bits), Expect = 1.5e-58, Sum P(5) = 1.5e-58
  Identities = 22/28 (78%), Positives = 22/28 (78%), Strand = Minus / Plus

15
```
Query:   256 TCCTGCCTTTGCAGAATTATTCCATTAT 229
             ||||| | || ||||||||||||| ||
Sbjct:   193 TCCTCCTTTCACAGAATTATTCCAGGAT 220
```